

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/586,978
Source: TFWP
Date Processed by STIC: 08/03/2006

ENTERED



IFWP

RAW SEQUENCE LISTING DATE: 08/03/2006
PATENT APPLICATION: US/10/586,978 TIME: 09:46:39

Input Set : F:\SEQLIST.TXT
 Output Set: N:\CRF4\08032006\J586978.raw

3 <110> APPLICANT: Kohonen-Corish, Maija
 5 <120> TITLE OF INVENTION: Methods of diagnosing colorectal cancer and reagents
 therefor
 7 <130> FILE REFERENCE: RICE-029
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/586,978 (Pg-6)
 C--> 9 <141> CURRENT FILING DATE: 2006-07-20
 9 <150> PRIOR APPLICATION NUMBER: AU 2004900340
 10 <151> PRIOR FILING DATE: 2004-01-23
 12 <150> PRIOR APPLICATION NUMBER: US 60/540,662
 13 <151> PRIOR FILING DATE: 2004-01-29
 15 <150> PRIOR APPLICATION NUMBER: PCT/AU2005/000077
 16 <151> PRIOR FILING DATE: 2005-01-24
 18 <160> NUMBER OF SEQ ID NOS: 46
 20 <170> SOFTWARE: PatentIn version 3.3
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 4181
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (221)..(2707)
 32 <400> SEQUENCE: 1

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37	tgtggcagaa	gggaccaagg	agtggatatt	gagcctgtga	agtccaaactc	ttaagctccg	180	
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41					1	5		
43	gcc atg	aaa tat	gga aac	gac tcc	tcg gcc	gag ctg agt	gag ctc cat	283
44	Ala Met	Lys Tyr	Gly Asn	Asp Ser	Ser Ala	Glu Leu	Ser Glu Leu His	
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47	tca gca	gcc ctg	gca tca	cta aag	gga gat	ata gtg gaa	ctt aat aaa	331
48	Ser Ala	Ala Leu	Ala Ser	Leu Lys	Gly Asp	Ile Val	Glu Leu Asn Lys	
49	25			30		35		
51	cgt ctc	cag caa	aca gag	agg gaa	cg gac	ctt ctg	gaa aag aaa ttg	379
52	Arg Leu	Gln Gln	Thr Glu Arg	Glu Arg Asp	Leu Leu	Glu Lys Lys	Leu	
53	40			45		50		
55	gcc aag	gca cag	tgc gag	cag tcc	cac ctc	atg aga	gag cat gag gat	427
56	Ala Lys	Ala Gln	Cys Glu	Gln Ser	His Leu	Met Arg	Glu His Glu Asp	
57	55			60		65		
59	gtc cag	gag cga	acg acg	ctt cgc	tat gag	gaa cgc	atc aca gag ctc	475
60	Val Gln	Glu Arg	Thr Thr	Leu Arg	Tyr Glu	Glu Arg	Ile Thr Glu Leu	
61	70			75		80		85
63	cac agc	gtc att	gcg gag	ctc aac	aag aag	ata gac	cgt ctg caa ggc	523

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65				90					95						100		
67	acc	acc	atc	agg	gag	gaa	gat	gag	tac	tca	gaa	ctg	cga	tca	gaa	ctc	571
68	Thr	Thr	Ile	Arg	Glu	Glu	Asp	Glu	Tyr	Ser	Glu	Leu	Arg	Ser	Glu	Leu	
69				105					110						115		
71	agc	cag	agc	caa	cac	gag	gtc	aac	gag	gac	tct	cga	agc	atg	gac	caa	619
72	Ser	Gln	Ser	Gln	His	Glu	Val	Asn	Glu	Asp	Ser	Arg	Ser	Met	Asp	Gln	
73				120					125						130		
75	gac	cag	acc	tct	gtc	tct	atc	ccc	gaa	aac	cag	tct	acc	atg	gtt	act	667
76	Asp	Gln	Thr	Ser	Val	Ser	Ile	Pro	Glu	Asn	Gln	Ser	Thr	Met	Val	Thr	
77				135					140						145		
79	gct	gac	atg	gac	aac	tgc	agt	gac	ctg	aac	tca	gaa	ctg	cag	agg	gtg	715
80	Ala	Asp	Met	Asp	Asn	Cys	Ser	Asp	Leu	Asn	Ser	Glu	Leu	Gln	Arg	Val	
81	150			155					160						165		
83	ctg	aca	ggg	ctg	gag	aat	gtt	gtc	tgc	ggc	agg	aag	aag	agc	agc	tgc	763
84	Leu	Thr	Gly	Leu	Glu	Asn	Val	Val	Cys	Gly	Arg	Lys	Lys	Ser	Ser	Cys	
85				170					175						180		
87	agc	ctc	tcc	gtg	gcc	gag	gtg	gac	agg	cac	att	gag	cag	ctc	acc	aca	811
88	Ser	Leu	Ser	Val	Ala	Glu	Val	Asp	Arg	His	Ile	Glu	Gln	Leu	Thr	Thr	
89				185					190						195		
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92	Ala	Ser	Glu	His	Cys	Asp	Leu	Ala	Ile	Lys	Thr	Val	Glu	Glu	Ile	Glu	
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95	ggg	gtg	ctt	ggc	cg	gt	tg	gt	gac	agg	cac	tt	g	g	gg	t	907
96	Gly	Val	Leu	Gly	Arg	Asp	Leu	Tyr	Pro	Asn	Leu	Ala	Glu	Glu	Arg	Ser	
97				215					220						225		
99	cgg	tgg	gag	aag	gag	ctg	gct	ggg	ctg	agg	gaa	gag	aat	gag	agc	ctg	955
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104	Thr	Ala	Met	Leu	Cys	Ser	Lys	Glu	Glu	Glu	Leu	Asn	Arg	Thr	Lys	Ala	
105				250					255						260		
107	acc	atg	aat	gcc	atc	cg	g	g	g	g	ctc	cg	agg	cg	gt	ct	1051
108	Thr	Met	Asn	Ala	Ile	Arg	Glu	Glu	Arg	Asp	Arg	Leu	Arg	Arg	Arg	Val	
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111	aga	gag	ctt	caa	act	cga	cta	cag	agc	gt	g	cc	aca	gg	ccc	tcc	1099
112	Arg	Glu	Leu	Gln	Thr	Arg	Leu	Gln	Ser	Val	Gln	Ala	Thr	Gly	Pro	Ser	
113				280					285						290		
115	agc	cct	ggc	cgc	ctc	act	tcc	acc	aac	cgc	ccg	att	aac	ccc	agc	act	1147
116	Ser	Pro	Gly	Arg	Leu	Thr	Ser	Thr	Asn	Arg	Pro	Ile	Asn	Pro	Ser	Thr	
117				295					300						305		
119	ggg	gag	ctg	agc	aca	agc	agc	agc	aat	gac	att	ccc	atc	gcc	aag		1195
120	Gly	Glu	Leu	Ser	Thr	Ser	Ser	Ser	Asn	Asp	Ile	Pro	Ile	Ala	Lys		
121	310			315					320						325		
123	att	gct	gag	agg	gt	g	a	g	c	t	a	g	t	c	t	ca	1243
124	Ile	Ala	Glu	Arg	Val	Lys	Leu	Ser	Lys	Thr	Arg	Ser	Glu	Ser	Ser	Ser	
125				330					335						340		
127	tct	gat	cg	cca	gtc	ctg	ggc	tca	gaa	atc	agt	agc	ata	ggg	gta	tcc	1291
128	Ser	Asp	Arg	Pro	Val	Leu	Gly	Ser	Glu	Ile	Ser	Ser	Ile	Gly	Val	Ser	

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132	Ser Ser Val Ala Glu His Leu Ala His Ser Leu Gln Asp Cys Ser Asn			
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135	atc caa gag att ttc caa aca ctc tac tca cac gga tct gcc atc tca			1387
136	Ile Gln Glu Ile Phe Gln Thr Leu Tyr Ser His Gly Ser Ala Ile Ser			
137	375	380	385	
139	gaa agc aag att aga gag ttt gag gtg gaa aca gaa cggtcg aat agc			1435
140	Glu Ser Lys Ile Arg Glu Phe Glu Val Glu Thr Glu Arg Leu Asn Ser			
141	390	395	400	405
143	cgg att gag cac ctc aaa tcc caa aat gac ctc ctg acc ata acc ttg			1483
144	Arg Ile Glu His Leu Lys Ser Gln Asn Asp Leu Leu Thr Ile Thr Leu			
145	410	415	420	
147	gag gaa tgt aaa agc aat gct gag agg atg agc atg ctg gtg gga aaa			1531
148	Glu Glu Cys Lys Ser Asn Ala Glu Arg Met Ser Met Leu Val Gly Lys			
149	425	430	435	
151	tac gaa tcc aat gcc aca qcg ctg agg ctg gcc ttg cag tac agc gag			1579
152	Tyr Glu Ser Asn Ala Thr Ala Leu Arg Leu Ala Leu Gln Tyr Ser Glu			
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155	cag tgc atc gaa gcc tac gaa ctc ctc ctg gca gag agt gag			1627
156	Gln Cys Ile Glu Ala Tyr Glu Leu Leu Ala Leu Ala Glu Ser Glu			
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159	cag agc ctc atc ctg ggg cag ttc cga gcg ggc gtg ggg tcc tcc			1675
160	Gln Ser Leu Ile Leu Gly Gln Phe Arg Ala Ala Gly Val Gly Ser Ser			
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163	cct gga gac cag tcg ggg gat gaa aac atc act cag atg ctc aag cga			1723
164	Pro Gly Asp Gln Ser Gly Asp Glu Asn Ile Thr Gln Met Leu Lys Arg			
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167	gct cat gac tgc cgg aag aca gct gag aac gct gcc aag gcc ctg ctc			1771
168	Ala His Asp Cys Arg Lys Thr Ala Glu Asn Ala Ala Lys Ala Leu Leu			
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171	atg aag ctg gac ggc agc tgt ggg gga gcc ttt gcc gtg gcc ggc tgc			1819
172	Met Lys Leu Asp Gly Ser Cys Gly Ala Phe Ala Val Ala Gly Cys			
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175	agc gtg cag ccc tgg gag agc ctt tcc tcc aac agc cac acc agc aca			1867
176	Ser Val Gln Pro Trp Glu Ser Leu Ser Ser Asn Ser His Thr Ser Thr			
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179	acc agc tcc aca gcc agt agt tgc gac acc gag ttc act aaa gaa gac			1915
180	Thr Ser Ser Thr Ala Ser Ser Cys Asp Thr Glu Phe Thr Lys Glu Asp			
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183	gag cag agg ctg aag gat tat atc cag cag ctc aag aat gac agg gct			1963
184	Glu Gln Arg Leu Lys Asp Tyr Ile Gln Gln Leu Lys Asn Asp Arg Ala			
185	570	575	580	
187	gcg gtc aag ctg acc atg ctg gag ctg gaa agc atc cac atc gat cct			2011
188	Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser Ile His Ile Asp Pro			
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191	ctc agc tat gac gtc aag cct cgg gga gac agc cag agg ctg gat ctg			2059
192	Leu Ser Tyr Asp Val Lys Pro Arg Gly Asp Ser Gln Arg Leu Asp Leu			
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197 615 620 625	
199 gcc gag ttg aag gcc cag ctc tac cta ctg gag aaa gag aag aag gcc	2155
200 Ala Glu Leu Lys Ala Gln Leu Tyr Leu Leu Glu Lys Glu Lys Lys Ala	
201 630 635 640 645	
203 ctg gag ctg aag ctg agc acg cgg gag gcc cag gag cag gcc tac ctg	2203
204 Leu Glu Leu Lys Leu Ser Thr Arg Glu Ala Gln Glu Gln Ala Tyr Leu	
205 650 655 660	
207 gtg cac att gag cac ctg aag tcc gag gtg gag gag cag aag gag cag	2251
208 Val His Ile Glu His Leu Lys Ser Glu Val Glu Glu Gln Lys Glu Gln	
209 665 670 675	
211 cgg atg cga tcc ctc agc tcc acc agc agc ggc agc aaa gat aaa cct	2299
212 Arg Met Arg Ser Leu Ser Ser Thr Ser Ser Gly Ser Lys Asp Lys Pro	
213 680 685 690	
215 ggc aag gag tgt gat gct gcc tcc cca gct ctg tcc cta gct gaa	2347
216 Gly Lys Glu Cys Ala Asp Ala Ala Ser Pro Ala Leu Ser Leu Ala Glu	
217 695 700 705	
219 ctc agg aca acg tgc agc gag aat gag ctg gct gcg gag ttc acc aac	2395
220 Leu Arg Thr Thr Cys Ser Glu Asn Glu Leu Ala Ala Glu Phe Thr Asn	
221 710 715 720 725	
223 gcc att cgt cga gaa aag aag ttg aag gcc aga gtt caa gag ctg gtg	2443
224 Ala Ile Arg Arg Glu Lys Lys Leu Lys Ala Arg Val Gln Glu Leu Val	
225 730 735 740	
227 agt gcc ttg gag aga ctc acc aag agc agt gaa atc cga cat cag caa	2491
228 Ser Ala Leu Glu Arg Leu Thr Lys Ser Ser Glu Ile Arg His Gln Gln	
229 745 750 755	
231 tct gca gag ttc gtg aat gat cta aag cgg gcc aac agc aac ctg gtg	2539
232 Ser Ala Glu Phe Val Asn Asp Leu Lys Arg Ala Asn Ser Asn Leu Val	
233 760 765 770	
235 gct gcc tat gag aaa gca aag aaa aag cat caa aac aaa ctg aag aag	2587
236 Ala Ala Tyr Glu Lys Ala Lys Lys His Gln Asn Lys Leu Lys Lys	
237 775 780 785	
239 tta gag tcg cag atg atg gcc atg gtg gag aga cat gag acc caa gtg	2635
240 Leu Glu Ser Gln Met Met Ala Met Val Glu Arg His Glu Thr Gln Val	
241 790 795 800 805	
243 agg atg ctc aag caa aga ata gct ctg cta gag gag gag aac tcc agg	2683
244 Arg Met Leu Lys Gln Arg Ile Ala Leu Leu Glu Glu Glu Asn Ser Arg	
245 810 815 820	
247 cca cac acc aat gaa act tcg ctt taatcagcac tcacgcaccc gagttctgcc	2737
248 Pro His Thr Asn Glu Thr Ser Leu	
249 825	
251 catggaaagt aaactgcagc aggccactgg ggacagaagg gcccattac ttgttggag	2797
253 gggaggaaa gggaggctg cgaggtaggt cggcacttg acaatggagt gccccaaactc	2857
255 aacccttggg gtgactggcc atggtgacat tgtggactgt atccagaggt gccccgtctt	2917
257 ccctcctggg cccacaacag cgtgtaaaca catttctgt gcctgcttag cagagcctcg	2977
259 ttctgtctt cagcaactac tctccccctc ctcttcttgt ctggcggctg tgcatcagtg	3037
261 ggatcccaga catttgttc tgtaagatt tccattgtat cctcttttg gtatgtctg	3097
263 ggctcatctt ctagaatctc gtttctcctc tttcctcctg cttcatggaa aacagacct	3157

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275	ctccctctca	gtggagcctt	attaatatcc	aagacttaga	gctggaaatc	tttttgatac	3517									
277	ctgttagtgg	actaaaattc	tgtcaggggt	ttcttcaaga	gctgagaaac	attattagca	3577									
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291	aaacaaattc	attattctt	ttcagtttt	cctcttctct	ctcagttcta	cactgataca	3997									
293	cttgaaggac	catttactgt	tttttctgt	agcaccagag	aatccatcca	aagttcccta	4057									
295	tgaaaaatgt	gttccattgc	catagctgac	tacaaattaa	agttgaggag	gtttctgcat	4117									
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322					50					55						60
325	Arg	Glu	His	Glu	Asp	Val	Gln	Glu	Arg	Thr	Thr	Leu	Arg	Tyr	Glu	Glu
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330					85					90						95
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346					145					150						160
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350					165					170						175
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 9521

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2947 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:9467